



Improving the history of health and fertility traits in dairy cows

Duration: 2016 – 2018

Highlights

- Dairy cattle productivity is influenced by the ways in which the animals are managed and their genetic potential. Through genetic improvement (traditional and genomic), we aim to improve performance by selecting the highest-performing versions of the genes. The traditional approach is to mate the highest-producing animals without taking DNA into account, while genomics aims to select the DNA sequences that are associated with animals exhibiting the highest productivity levels.
- The general model involves having two copies of the best version of the gene, representing the best genetic combination. However, it has been found that certain traits react better to the cross-breeding of different species, most notably traits associated with health and fertility. This means that, for certain traits, the best combination is to have two different versions.
- Dairy production in Quebec and Canada is not based on the cross-breeding of species to promote genetic heterogeneity. Furthermore, it is contraindicated to aim for genome-wide diversification (all of the DNA that is found in each cell) because this would counter the genetic gains made in the last 40 years.
- In this project, we propose developing a genomic analysis tool that would leverage the genetic variability present in the Holstein species to diversify specific regions of the genome known to be involved in health and fertility traits. The objective is to improve these traits that respond poorly to current selection processes by drawing from the species' existing genetic diversity.

Objectives

- Our hypothesis is that the diversification of specific regions of the genome will help improve health and fertility traits.
- The objectives are to develop a genomic analysis tool that will allow us to generate a genetic diversity score, which we can then apply in the assessment of an animal's genetic heritage or to estimate diversification potential through mating.

To do so, we must:

- Identify the regions known to influence the health and fertility of dairy cattle.
- Choose targets.
- Develop a genome analysis tool.
- Program the interface to make it easy to use.
- Test the tool with genomic data.

Results and potential benefits

Canada has an excellent reputation in regards to the genetic quality of its dairy herds. The driving force of this efficiency in genetic improvement is the result of the amount and precision of performance data collected on farms. Since 2009, genomic selection has complemented traditional genetics. The current model focuses on concentrating the good versions of genes, which decreases genetic diversity. A decrease in the number of bulls also greatly affects the species and has led to an uptick in inbreeding rates. It is known that it is more difficult to improve health and fertility traits. This is possibly because these traits are greatly influenced by the environment, in addition to involving a large number of genes that, individually, have very little influence. All dairy genetic selection has turned to genomics and, currently, rising above the rest is difficult because everyone is focusing on the same genetic combination. We believe that we can make a difference in the improvement of health and fertility traits by attempting to diversify regions of the genome that are known to be involved in these traits. By leveraging the species' existing genetic diversity, we will avoid the unfavourable case of interbreeding animals of different species. Given equal genetic values, an animal with a higher genetic diversity score will be better suited for production. So far, more than 99,652 regions of the genome that are known to be involved in bovine biological functions have been identified in the literature and correspond to 574 different traits. This information was sorted and structured in a database. As part of this project, 177 bulls from four genetics companies as well as 10 cows were genotyped. The genetic diversity for the targeted regions was calculated for each animal, and correlation values were calculated based on the genetic values associated with the different traits considered by the national genetic improvement program. The correlation values are high (0.34 to 0.51) for health and fertility traits and are low for production traits, suggesting that the targeted regions are not involved in these traits. A validation phase is ongoing using DNA from 200 cows that were shown to be healthy or susceptible to various health and fertility disorders. The ultimate objective is to improve health and fertility traits in these animals, which will improve their longevity and therefore reduce replacement costs.



Professionals trained

The project will allow for the training of:

- a master's student (**Alexandra Carrier**) who will be involved in the programming of the tool.
- a research professional (**Alexandre Bastien**) who will also be involved part-time in the programming and to assist the student.

Ultimately, these individuals will develop new skills in genomic analysis. These skills are greatly needed in Quebec if we would like to remain competitive in the field of genetic selection (all species combined).

For further information

This is an applied research project whose target public is mainly actors involved in genetic selection and dairy farmers. We will present our results at the Quebec Dairy Cattle Symposium and the Novalait Technological Forum, and we will produce an article for a journal read by dairy farmers (most likely Le producteur de lait québécois).

Financial contributions

Partnership for innovation in dairy production and dairy processing (EPI 2015-2019):

- Consortium de recherche et innovation en bioprocédés industriels au Québec
- Fonds de recherche du Québec – Nature et technologies
- Novalait

Total budget: \$186,706

Contact persons

Project supervisor:

Claude Robert

Animal Science Department
Centre de recherche en reproduction,
développement et santé intergénérationnelle
Institute of Nutrition and
Functional Foods (INAF)

Université Laval
Pavillon des services
2440 boul. Hochelaga
Quebec City (QC) G1V 0A6

418 656-2131 poste 12842
Claude.robert@fsaa.ulaval.ca